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ACGTTGACAC	AGGAATGAAG	AGTGTATTGG	CTGAATCTTC	AAGCAGAGGC	GATATTGACC	60
ATGTGCTTTT	TAAATTGGCC	TGCGTGACCC	GCCCCACTGG	TGTAAAAGAA	GAACCGGCCA	120
AAGGGAGGGC	CTGAAGGACC	TCCACAGGAG	TGTGAGCAGC	ACTGCTTCAG	CAACAAAGCC	180
TCAGGTCCAC	ATCTTGGGAA	GAAT	ATG GCC ACT TCC TGG GGG GCT GTC TTC			231
			Met Ala Thr Ser Trp Gly Ala Val Phe			
			1	5		
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG						279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln						
10	15		20	25		
CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT						327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn						
	30		35	40		
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT						375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr						
	45		50	55		
GGA ACT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG						423
Gly Thr Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln						
	60		65	70		
CTC CCC TTT CTG GAA GGT GAA ATT TTT GAT TCT GTG AAG CCG GGA CTT						471
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu						
	75		80	85		
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG						519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu						
	90		95	100	105	
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG						567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg						
	110		115	120		
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG						615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Pro Glu						
	125		130	135		
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT						663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn						
	140		145	150		
TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC						711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser						
	155		160	165		
TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG						759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln						
	170		175	180	185	
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT						807
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly						
	190		195	200		
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA						855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu						
	205		210	215		
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT						903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr						
	220		225	230		

Fig. 1

TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala 235 240 245	951
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His 250 255 260 265	999
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile 270 275 280	1047
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met 285 290 295	1095
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys 300 305 310	1143
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser 315 320 325	1191
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys 330 335 340 345	1239
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val 350 355 360	1287
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met 365 370 375	1335
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC Asp Leu Thr Tyr Ile Thr Ala Leu Lys Asp Gly Leu Gly Phe Ala 380 385 390	1383
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp 395 400 405	1431
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His 410 415 420 425	1479
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser 445 450 455	1575
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT Gly Lys Ala Trp Pro Glu Thr Arg 460 465	1629

Fig. 1 (cont'd.)

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TAGATGAGTC	TTGCTCTTGA	GCCTAGTGAT	TTGGGCTTCA	ATGATTTGCA	CATCTAATGT	1689
GAATAGCTCC	TAACCACTTG	GTGGGTGCAT	GGCTGGCACC	AGACTGTAAA	TCTTTTGGGA	1749
TTCTTTGTAC	AGAGTCCTGC	AAAGGAAAAA	AGAGAAAAGG	TTTGGAATC	CATGCTAGAT	1809
TGCGAGTTCA	GAGACAGGTC	CCTGGGGACC	AAAGAACAA	CTCGTTTCAA	CCCTTGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTTGC	TTATAAGCTG	ATTTACTGAA	ATCCCATAAC	1929
CCATCAATGC	TGTTAATTTT	TTCTTCCTA	CCCTTATTAC	ATTCCCTACC	CTAAAAGCCT	1989
GGGGGAAATA	CCTGGTTTTG	CTCCCATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GTATTAGAAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATTT	AAAGCTTAAA	2109
AAAAAAAAAA						2119

Fig. 1 (cont'd.)

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peaNTase 1 ----KELLKKTTFKTSKAISSOYIGONMLTSRTKPKQZGIGSAYVFDAGSTGSR
potapyrase 1 ELNQNSHTFIDLHMLVLLSLKWNACQPERRHLSHSE..HYAVHFDAGSTGSR
mNTase 1 KATSWGATFMDIACWGSYFYRSCQWTFEGYPLSSMCFENVYAGTFVCHFDAGSTGSR
yGDPase 1 KTKPKIIFTHYNDERFGYLDQKATPCNYPFLADAKSKSQTSQTCSEHKKVTHFDAGSTGSR

peaNTase 57 LHVYHENONDDLPKIGKGVETKKTTPGLSSYANPPOANKSLIPLLQABDUVVDLQOP
potapyrase 59 VHVFPDDEKLLAPICNNIEYFMAEPGLSSYADDPKAAANSLPPLLCAGVUPORHQS
mNTase 61 LHVYTFVORTAGQLPFLGEGEPDGVKPGLSAYVHOPKOGAENYQBLLEVARDSIPRSHWE
yGDPase 61 VHTYKRFDVCTG..PPTLLDEKFDMLPGLSSEDTGCVGAANSILPPLKAVANNYVFIKARS

peaNTase 117 STVWRGATAGLRLNCDASEKILQSVRDMSNRSTF..NVQFPAVSIIDGTOEGSYLVVT
potapyrase 119 STPLEGATAGLRMLKGDNAENILOAVNNLYKNOSTF..HKKQDMVTHLDGTOEGSYLVAN
mNTase 121 STVWRGATAGLRMLPEQAQALLLEVEEFKN.SPF..LVPEQGVSIHDSYEGILANVT
yGDPase 119 CDPVAKKATAGLRMLGDASKSNLPSAVRDELEKDYFPPYVRQDGVSIHDSYEGVLAWHI

peaNTase 176 VNYALGNLGRKNTK..TVGVIDLGGGSVONAXAVSKKFAKNAPKMAADGMDPYKKKVVKQ
potapyrase 178 INYLLGNLGRKDKS..TATIDLGGGSVONAXAVISNQCBAKAEQNEGG..REYVQKKEHMS
mNTase 179 VNYLLTGLHGGQKE..TVGTIDLGGGSVONAXAVISNQCBAKAEQNEGG..REYVQKKEHMS
yGDPase 179 THYLLGNLGRKNTK..TVGVIDLGGGSVONAXAVSKKFAKNAPKMAADGMDPYKKKVVKQ

peaNTase 234 IPDOLYVHSYLFEGREASRAEILKL.....PFRSPNPCLLAGTNGIY
potapyrase 235 KDYNLYVHSYLYMIGOLAGRAEIPKA.....GKNSNPCALDEGCDGY
mNTase 232 STEKLYTHSYLGFGLKARLALHGA.....LEAKGT.....DCHTFAS
yGDPase 234 ENNTLYIQFSLHGYGLNEGRNKVNSVLVENALKDGKILKGDNTKQKLSPCPPFKVNTN

peaNTase 276 TVSGEPKATAYTSN.....NANENKUTIRKALHONYPQPYQNCTEGGMWNGCGGN...
potapyrase 277 SYGQYDYNVKAIPKKS.....SNKRCRSTREKALHONKCHNTEGGMWNGCGGN...
mNTase 270 KCEPRNLEAEWIFGGV.....KYQYGGHGGEGMGTIFCYAKVLRVQCKDHQPEEVR...
yGDPase 294 EKYTLSEKREYITIDFIGPDEPFGAQCRFTDQIENKKKQCGSPFCSENGVHQPSLVRTFK

peaNTase 328 GQKNCFASSSRYLPEDTGHVDASTPNFMDREYDIEKAKEACALNEPDKKSTYFDDKE
potapyrase 329 GQKNIBASSFEDICAQVGHVDAKFSADAKPLQYLNAAHVACQNVADKSLFPKTRQK
mNTase 322 GSAFYAPSYVDRAADTHEIDYE..KGGVLEVEDEPRKAREVCH..DLGSFSSGS...
yGDPase 354 ESNDLYIFSYEDRGRPLGMLPFLNPNLNDLARIVCKGPEWREVEHCHAGS...HDEL

peaNTase 388 NGASYVCHDLIYQVLLVDGFGCHDLOKHTGKREIEYQDAIVLAAWPLGNAYKALSALPK
potapyrase 389 NM..PFLCHDLIYVTHAVDGGCHDNEHTVHIDVOYKYLUGAANPLCCADIPYSRTN
mNTase 374 ...FLCHDLIYVTHAVDGGCHDNEHTVHIDVOYKYLUGAANPLCCADIPYSRTN
yGDPase 411 ESDBHFCDDSTQVSLKHTGQDPLQREHRTGKRIANNS...IGWCLGASHPPZLKNDDN

peaNTase 448 FERTMYFV-----
potapyrase 448 KIRYASH-----
mNTase 430 PSSTAEACISEPVFSQEGVDSETFSDLSGKANPETR*
yGDPase 467 KCKKQSA-----

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FIG. 2

[illegible]

ACR II

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CD39      47  VGVSYMIK L VVDC ERS... S C C...
ratCD39   47  VGVSYMIK L VVDC ERS... S C C...
CD392     47  VGVSYMIK L VVDC ERS... S C C...
chickATPase 47  SSSD L K L EEC SCARD...
peanATPase 46  SSSD L K L EEC SCARD...
potATPase  46  SSSD L K L EEC SCARD...
yADP1     44  SSSD L K L EEC SCARD...
ATPase    46  SSSD L K L EEC SCARD...
h13D352   46  SSSD L K L EEC SCARD...
catATPase 51  SSSD L K L EEC SCARD...
vncD      61  SSSD L K L EEC SCARD...

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ACR III

[illegible]

ACR IV

F16.3

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GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGGCCCG GCCGGGGCGG GGGAGCCCAA 60
 AAGACCGGCT GCCGCCTGCT CCCCAGAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC 120
 GCGCGGTGCA TGGAAATGGG TATGTGAATG AAAAAAGGTA TCCGTTATGA AACTTCCAGA 180
 AAAACGAGCT ACATTTTCA GCAGCCGCAG CACGGTCCTT GGCAACAAG G ATG AGA 237
 Met Arg
 1

AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC 285
 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
 5 10 15

CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG 333
 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
 20 25 30

CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC 381
 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
 35 40 45 50

CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT 429
 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
 55 60 65

GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC 477
 Ala Asp Gly His Glu Val Phe Tyr Phe Ile Met Phe Asp Ala Gly Ser
 70 75 80

ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA 525
 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
 85 90 95

ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT 573
 Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
 100 105 110

TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA 621
 Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
 115 120 125 130

CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC 669
 Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
 135 140 145

ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA 717
 Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly
 150 155 160

GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA 765
 Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala
 165 170 175

TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA 813
 Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr
 180 185 190

GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC 861
 Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
 195 200 205 210

TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA 909
 Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
 215 220 225

FIG. 4

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GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln 230 235 240	957
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr 245 250 255	1005
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala 260 265 270	1053
CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA Arg Leu Ala Ile Leu Gly Val Glu Gly Gln Pro Ala Lys Asp Gly 275 280 285 290	1101
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp 295 300 305	1149
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310 315 320	1197
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325 330 335	1245
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340 345 350	1293
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355 360 365 370	1341
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375 380 385	1389
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390 395 400	1437
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro 405 410 415	1485
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420 425 430	1533
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435 440 445 450	1581
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT Gln Lys Ser Pro Ala Ser 455	1637
GTGTGTCTGC ATAAACCCTC CTGTCTCTGGA CGTGACTTCA TCCTGAGGAG CCACAGCACA GGCCGTGCTG GCACTTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCCC TGGCATCAGC CTCTTCCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC	1697 1757 1817

Fig. 4 (cont'd.)

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AATGCCACCT	GTCTGCC TGG	GCTCCAAGTG	GGCAGGACCA	GGACAGAACC	ACAGGCACAC	1877
ACTGAGGGGG	CAGTGTGGCT	CCTCGCTGT	CCCATCCCCA	TGCCCCGTCC	GCGGGGCTGT	1937
GGCTGCTGCT	GTGCATGTCC	TGCGATGGT	AGGCTTGTCT	CCCAGCTGCT	CAGTTTCTCT	1997
CCCAGGGCAG	AGCTCCCCCT	CCTGCAAGAG	TCTGGGAGGT	GGTGACGGT	GTCTTGGCTG	2057
CTCTGGGGAA	GCCGAGGGAC	AGCCATAACA	CCCCCGGAG	AGTAGGCTG	GGCGGCACCA	2117
CTGGGAACCT	TGGACTTGG	TGTGTTTGT	CTTCTTGGG	TATGAATGT	TGAGTTCACC	2177
CAGAGGCGCT	CTCTCCTCAC	ACATTGTGTG	TTTTGGGTT	AATGATGAG	GGAGACACCT	2237
CTTCATAGAC	GGCAGGTGAC	CACCTTTTCA	GGAGTCTCCC	AGCATGGGCG	GATGCCGGGC	2297
ATGAGCTGCT	GTAACATCTT	TGTGGCTGTG	CTGCTTGAGT	GACGTCTCTG	TCGTGTGGGT	2357
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TC7GGACACC	AAC7GTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GAGCTGTTCC	CGCTAGCCCA	GGGCCATGTC	TTAGGTGCAG	2477
CTGTGCCACG	GGTCAGCTGA	GCCACAGTCC	CAGAACAACG	CTCTCGGTGT	CTCGGGCCAC	2537
CATCCGCCCC	CCTCGGGCTG	ACCCCACTC	CTCCATGAC	AGTGTGAGCC	CCGGGGCGTG	2597
CATCTGCTCT	AGTGTGGCGT	CAGTGTCCGG	GCTGAGCCCT	TTGAGCTGCT	TCAGTGAATG	2657
TACAGTGCCC	GGCACGAGCT	GAACCTCATG	TGTTCCACCT	CCAAATAAAG	GTTGACAGGG	2717
GCTTCTCTCT	CAAAAAAATA	AAAAAATAAA	AAAAAATAAA	AAAAA		2767

FIG. 4 (cont'd)

[illegible]

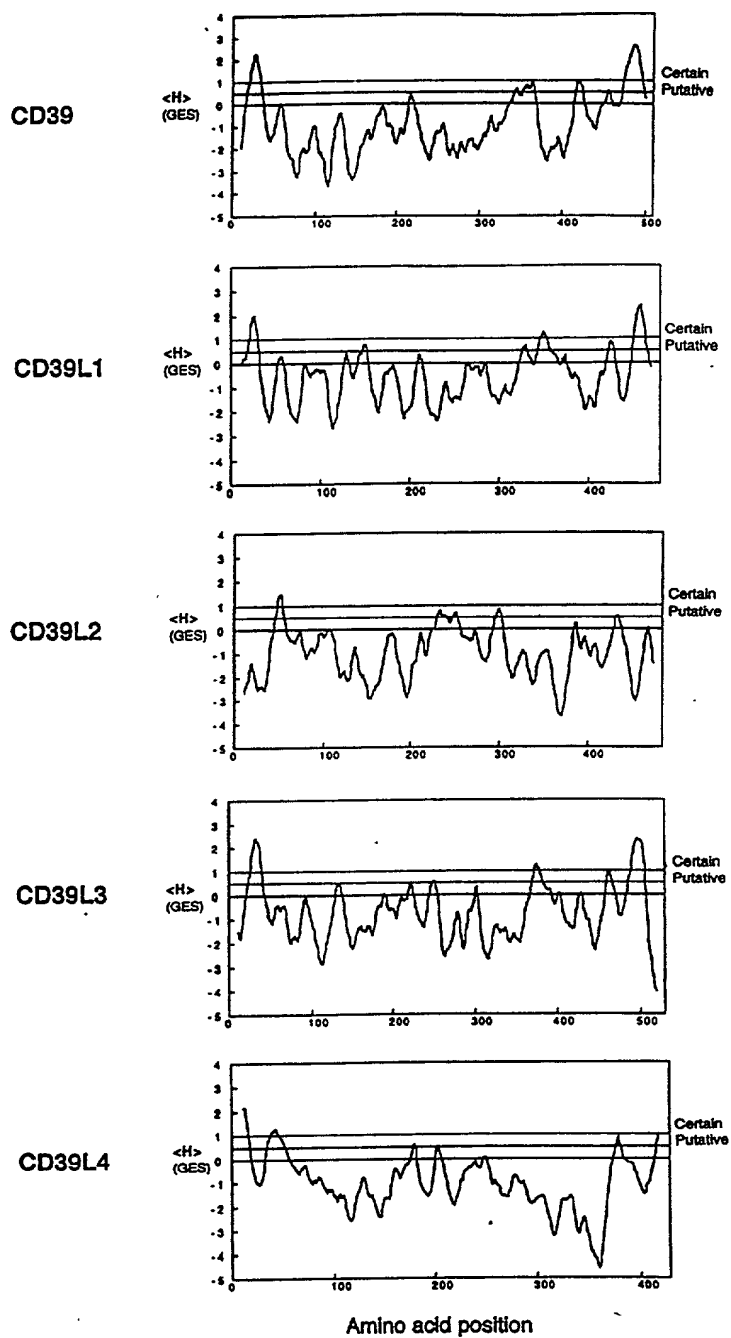


FIG. 5

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ACCCACGCGT CTGGCCGCGG GCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG	60
CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT	112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys	
1 5 10	
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC	160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala	
15 20 25	
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC	208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val	
30 35 40	
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT	256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly	
45 50 55	
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA	304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln	
60 65 70	
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe	
75 80 85 90	
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	
95 100 105	
CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	
110 115 120	
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	
125 130 135	
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	
140 145 150	
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	
155 160 165 170	
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	

Fig. 6

ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr 235 240 245 250	832
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu 255 260 265	880
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys 270 275 280	928
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe 285 290 295	976
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro 300 305 310	1024
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp 315 320 325 330	1072
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala 335 340 345	1120
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys 350 355 360	1168
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser 365 370 375	1216
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser 380 385 390	1264
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu 395 400 405 410	1312
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 415 420 425	1360
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 430 435 440	1408
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 445 450 455	1456
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu 460 465 470	1504
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Val Phe Val Gly Thr 475 480 485 490	1552

FIG. 6 (cont'd.)

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GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA TGGC 1703
Asp His Ala Val Asp Ser Asp
525

TGCTTAGAGT	CAGCCTGGGT	GGCACCAGGC	AATGCAGGTG	AAGTGGCTGC	CTTCAGGAAA	1763
TACCACTAAT	TAAATCAAAA	CACCTAGGTT	ACGTGCCCTCT	CAAAATACGA	TTTCTGCCAC	1823
AGCACTCTTC	AGGCATCCCC	TTGGCTATTCT	TGGTCATATT	GTTCCTCAGA	GACCCTCACTA	1883
CCCACATGCT	GATCTATTGG	GGAAACAGTA	AGAGACAGGC	CACATAAGGTC	AGGCTCTTTA	1943
TATTAAGTTT	CCCAGAGGAA	GAGTAAGATTG	AGAAGGTATC	AGTTTAATGT	TGAAGAATTG	2003
ACCTCAGGGC	TCAGTTTPCCA	TTTCCCTCCC	TCAGTATTCT	TCCTGGCAAG	ATACCCATTA	2063
AGCAATTTCG	CAATCAGAAAT	CTCATTTTAT	AGTTTTCCTCC	AGTTGGTCTTT	AACTAAGACT	2123
TTCTTGTAGC	AAFTCTCGTA	GCAGTGAACC	CCCTCAGATC	ATGATAAATAT	AGTATCTGGG	2183
GGAGAAGACT	TACTTCCTTC	AGGGCAGCAG	CCACAGCCAG	GCTTCTGTCA	TACAGGTAGA	2243
TTCCGGAAGCA	CAGAGACATA	AAAAGGCTCT	CCCGAGAAAAC	TATGATGACT	TCCTCAAGTG	2303
GAATTCCCAC	TTAGGGCTCT	GGTCACTAGA	TTGCAAACTG	TTGTATTGTC	ATCATCTCCA	2363
TCTCACCATT	GTATTGCTAT	GCCCTCCCAT	AAAAACACAT	TGATCCCTAG	CAAGATTATT	2423
GCATTCCAGA	TTTATCTGCC	TTTGTACAGC	TTTTGCTTAG	CAAAAGGGCTG	ACTTTCCATT	2483
GTTATCTATG	TGTATATATT	TTTGTCAACA	TTCCCAACAG	TATACTTGAT	GTTGTCCATG	2543
AACGATACAT	CTACTCTATG	ATTTACTAAC	CAATTAACCT	CCAGATCACT	AGACCTCTCT	2603
CGCTAGTAGT	CATAGGTTCT	CAGTTTGGGG	AAAGAAAAGG	ACCGATCAGG	AAATATTATT	2663
TCCAAAGTCG	AATGAGAAAG	AACTCCAGCA	AATCCAATGG	CTACAAACTA	AAAATCAGCA	2723
TTATTTCATA	TGCTGTTCCT	TTAGCTGAAT	ATGGAATAAA	GACTATTAT	TTTATTTTGA	2783
AAAAAAAAAA	AAAA					2797

F1 G. 6 (cont'd.)

[illegible]

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FIG. 7

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ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC 1008
 Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr
 240 245 250

CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT 1056
 Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser
 255 260 265 270

GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG 1104
 Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val
 275 280 285

AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC 1152
 Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro
 290 295 300

TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA 1200
 Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro
 305 310 315

GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC 1248
 Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp
 320 325 330

CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA 1296
 Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu
 335 340 345 350

AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG 1344
 Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu
 355 360 365

GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC 1392
 Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr
 370 375 380

ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC 1440
 Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val
 385 390 395

TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG 1488
 Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu
 400 405 410

GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC 1539
 Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
 415 420 425

GTACTTCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGAGA GAGCACTTAG 1599
 TTTCTGAACT AGTCTGGGAC ATCCTGGACT TGAGCCTAGA GATTTAGGTT TAATTAATTT 1659
 TACACATCTA ATGTGAACTG CTGCCTAACC ACTCAAGAGT ACACAGCTGG CACCAGAGCA 1719
 TCACAGAGAG CCCTGTGAGC CAAAAAGTAT AGTTTGGAA CTTAACCTTG GAGTGAGAGC 1779
 CCAGGGACAG GTCCCTGGAA ACCAAAGAAA AATCGCATT CAACCCTTTG AGTGCCTCAT 1839
 TCCACTGAAT ATTTAAATTT TCCTCTTAAA TGGTAAACTG ACTTATTGCA ATCCCAAGAC 1899
 CCATCAATAT CAGTATTTT TCCTCCCTA TACAGTGCCC TGCCCACCCT TATCTGCACC 1959
 CACCTCCCCT GAAAAAGAGA GAAAAAATA AAAAAAATA 1998

FIG. 7 (cont'd.)

CD39L2 1 MKKGIRYETSRKTSYIFQQPQHGPWQTRMRKISHHGSRLVAKVATPLGQCVGVFIVVATK
 CD39L4 1 -----
 CD39L1 1 -----
 CD39L3 1 -----
 CD39 1 -----

CD39L2 61 KNEKATAGQFFETRAIPETRMGQOAE.SELGTAANGHEVYGLSDAGSGGFFVHVLG
 CD39L4 7 TVFFMLVVSCHSAASHKNOOTFFGCFSSKPCPRTVSAATLYGLEDAGSGGFFVHVLG
 CD39L1 1 ---MAGKYRPPFPAKATLADLDCVPTKVRPPKYGIVLDAGSSHTSSEVYK
 CD39L3 16 KANTREPHIATVRLGIVVLVSITQIHRQVLPPKYGIVLDAGSSHTSVVYVO
 CD39 7 SNKATFCSHMDGIGFETITAVIADAGLQFQKALPENVKYGIIVLDAGSSHTSEVYK

CD39L2 120 FT.KPPFRETPTREAFQVN.PG.SAYADVYKAOFFRELLVARODIPFDMKATPL
 CD39L4 67 FYQKMPGQLFIDIGVPCSVF.PG.SAYVDSKPAFAGLEVAVDSPRSMKRTPE
 CD39L1 58 SPAKENDTGIVGCHESCDVPCGRISYADHPSGLHOSVVCLEQALDDPPFTHATPL
 CD39L3 75 SPAKENDTGIVGCHESCDVPCGRISYADHPSGLHOSVVCLEQALDDPPFTHATPL
 CD39 67 SPAKENDTGIVGCHESCDVPCGRISYADHPSGLHOSVVCLEQALDDPPFTHATPL

CD39L2 178 YLCATAGHRLM...FGRKATL...KKE...K...SPLVGGDDCVSIR...
 CD39L4 126 YLCATAGHRLM...FGRKATL...KKE...K...SPLVGGDDCVSIR...
 CD39L1 114 YLCATAGHRLM...FGRKATL...KKE...K...SPLVGGDDCVSIR...
 CD39L3 135 YLCATAGHRLM...FGRKATL...KKE...K...SPLVGGDDCVSIR...
 CD39 127 YLCATAGHRLM...FGRKATL...KKE...K...SPLVGGDDCVSIR...

CD39L2 235 LQSSL.....LPGGSLVGMIDLGGSTQIFLPRVETLASSPCVLTALR
 CD39L4 183 LQSSL.....LPGGSLVGMIDLGGSTQIFLPRVETLASSPCVLTALR
 CD39L1 176 LQSSL.....LPGGSLVGMIDLGGSTQIFLPRVETLASSPCVLTALR
 CD39L3 193 LQSSL.....LPGGSLVGMIDLGGSTQIFLPRVETLASSPCVLTALR
 CD39 185 LQSSL.....LPGGSLVGMIDLGGSTQIFLPRVETLASSPCVLTALR

CD39L2 283 NPTKLYRISHLGLSLMARLA-LGTEGCPANQGLVSPCLSPSPKPEVLEH...VYR
 CD39L4 231 NPTKLYRISHLGLSLMARLA-LGTEGCPANQGLVSPCLSPSPKPEVLEH...VYR
 CD39L1 229 YGQVVEYTHSFLCYGRDQVLRQLASAGQ.....LQFPCMPRGESVYLCGVNOS
 CD39L3 248 YGQVVEYTHSFLCYGRDQVLRQLASAGQ.....LQFPCMPRGESVYLCGVNOS
 CD39 242 YGQVVEYTHSFLCYGRDQVLRQLASAGQ.....LQFPCMPRGESVYLCGVNOS

CD39L2 343 YGQVVEYTHSFLCYGRDQVLRQLASAGQ.....LQFPCMPRGESVYLCGVNOS
 CD39L4 290 YGQVVEYTHSFLCYGRDQVLRQLASAGQ.....LQFPCMPRGESVYLCGVNOS
 CD39L1 283 YGQVVEYTHSFLCYGRDQVLRQLASAGQ.....LQFPCMPRGESVYLCGVNOS
 CD39L3 307 YGQVVEYTHSFLCYGRDQVLRQLASAGQ.....LQFPCMPRGESVYLCGVNOS
 CD39 300 YGQVVEYTHSFLCYGRDQVLRQLASAGQ.....LQFPCMPRGESVYLCGVNOS

CD39L2 403 LQVQDFEIKAKYVCRLETQPSPPFCMDVYVLLQOR.PG.PRSKVKLTHRORVE
 CD39L4 350 LQVQDFEIKAKYVCRLETQPSPPFCMDVYVLLQOR.PG.PRSKVKLTHRORVE
 CD39L1 342 LQVQDFEIKAKYVCRLETQPSPPFCMDVYVLLQOR.PG.PRSKVKLTHRORVE
 CD39L3 367 LQVQDFEIKAKYVCRLETQPSPPFCMDVYVLLQOR.PG.PRSKVKLTHRORVE
 CD39 357 LQVQDFEIKAKYVCRLETQPSPPFCMDVYVLLQOR.PG.PRSKVKLTHRORVE

CD39L2 462 KSWALGAIPIHYDEGKSPK*-----
 CD39L4 410 KSWALGAIPIHYDEGKSPK*-----
 CD39L1 384 KSWALGAIPIHYDEGKSPK*-----
 CD39L3 418 KSWALGAIPIHYDEGKSPK*-----
 CD39 409 KSWALGAIPIHYDEGKSPK*-----

CD39L2 485 -----
 CD39L4 429 -----
 CD39L1 432 KSKOTFSEHVVVLLHLSGALLALGHHHROVHSLPSTI*-----
 CD39L3 478 KSKOTFSEHVVVLLHLSGALLALGHHHROVHSLPSTI*-----
 CD39 468 KSKOTFSEHVVVLLHLSGALLALGHHHROVHSLPSTI*-----

FIG. 8

2 ACR I

ACR II

ACR II

ACR III

ACR IV

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WILSON

YVHSYL
YVHSYL

Y: SYL

THSYL